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#12

RAW SEQUENCE LISTING

DATE: 11/13/2002

PATENT APPLICATION: US/09/898,234B

TIME: 15:47:18

Input Set : A:\98385Iseq.txt

Output Set: N:\CRF4\11132002\I898234B.raw

3 <110> APPLICANT: Hauptmann, Rudolph
4 Himmeler, Adolph
5 Maurer-Fogy, Ingrid
6 Stratowa, Christian
8 <120> TITLE OF INVENTION: TNF Receptors, TNF Binding Proteins and DNAs Coding for.
9 Them
11 <130> FILE REFERENCE: 98-385-I
13 <140> CURRENT APPLICATION NUMBER: 09/898,234B
14 <141> CURRENT FILING DATE: 2001-07-03
16 <150> PRIOR APPLICATION NUMBER: 09/525,998
17 <151> PRIOR FILING DATE: 2000-03-15
19 <150> PRIOR APPLICATION NUMBER: 08/383,676
20 <151> PRIOR FILING DATE: 1995-02-01
22 <150> PRIOR APPLICATION NUMBER: 08/153,287
23 <151> PRIOR FILING DATE: 1993-11-17
25 <150> PRIOR APPLICATION NUMBER: 07/821,750
26 <151> PRIOR FILING DATE: 1992-01-02
28 <150> PRIOR APPLICATION NUMBER: 07/511,430
29 <151> PRIOR FILING DATE: 1990-04-20
31 <160> NUMBER OF SEQ ID NOS: 97
33 <170> SOFTWARE: PatentIn Ver. 2.0
35 <210> SEQ ID NO: 1
36 <211> LENGTH: 1368
37 <212> TYPE: DNA
38 <213> ORGANISM: Homo sapiens
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44 <220> FEATURE:
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46 <222> LOCATION: (1)..(87)
48 <220> FEATURE:
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50 <222> LOCATION: (88)..(120)
51 <223> OTHER INFORMATION: portion of TNF-BP pro protein cleaved by
52 extracellular proteases following secretion
54 <220> FEATURE:
55 <221> NAME/KEY: misc_feature
56 <222> LOCATION: (606)..(633)
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58 extracellular proteases following secretion
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P6
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65 gag ctg ttg gtg gga ata tac ccc tca ggg gtt att gga ctg gtc cct   96
66 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
67           20           25           30
69 cac cta ggg gac agg gag aag aga gat agt gtg tgt ccc caa gga aaa   144
70 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
71           35           40           45
73 tat atc cac cct caa aat aat tcg att tgc tgt acc aag tgc cac aaa   192
74 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
75           50           55           60
77 gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag gat acg gac   240
78 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
79   65           70           75           80
81 tgc agg gag tgt gag agc ggc tcc ttc acc gct tca gaa aac cac ctc   288
82 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
83           85           90           95
85 aga cac tgc ctc agc tgc tcc aaa tgc cga aag gaa atg ggt cag gtg   336
86 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
87           100          105          110
89 gag atc tct tct tgc aca gtg gac cgg gac acc gtg tgt ggc tgc agg   384
90 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
91           115          120          125
93 aag aac cag tac cgg cat tat tgg agt gaa aac ctt ttc cag tgc ttc   432
94 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
95           130          135          140
97 aat tgc agc ctc tgc ctc aat ggg acc gtg cac ctc tcc tgc cag gag   480
98 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
99 145          150          155          160
101 aaa cag aac acc gtg tgc acc tgc cat gca ggt ttc ttt cta aga gaa   528
102 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
103           165          170          175
105 aac gag tgt gtc tcc tgt agt aac tgt aag aaa agc ctg gag tgc acg   576
106 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
107           180          185          190
109 aag ttg tgc cta ccc cag att gag aat gtt aag ggc act gag gac tca   624
110 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
111           195          200          205
113 ggc acc aca gtg ctg ttg ccc ctg gtc att ttc ttt ggt ctt tgc ctt   672
114 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
115           210          215          220
117 tta tcc ctc ctc ttc att ggt tta atg tat cgc tac caa cgg tgg aag   720
118 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
119 225          230          235          240
121 tcc aag ctc tac tcc att gtt tgt ggg aaa tgc aca cct gaa aaa gag   768
122 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
123           245          250          255
125 ggg gag ctt gaa gga act act act aag cbc ctg gcc cca aac cca agc   816
126 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser

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127          260          265          270
129 ttc agt ccc act cca ggc ttc acc ccc acc ctg ggc ttc agt ccc gtg 864
130 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
131          275          280          285
133 ccc agt tcc acc ttc acc tcc agc tcc acc tat acc ccc ggt gac tgt 912
134 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
135          290          295          300
137 ccc aac ttt gcg gct ccc cgc aga gag gtg gca cca ccc tat cag ggg 960
138 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
139 305          310          315          320
141 gct gac ccc atc ctt gcg aca gcc ctc gcc tcc gac ccc atc ccc aac 1008
142 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
143          325          330          335
145 ccc ctt cag aag tgg gag gac agc gcc cac aag cca cag agc cta gac 1056
146 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
147          340          345          350
149 act gat gac ccc gcg acg ctg tac gcc gtg gtg gag aac gtg ccc ccg 1104
150 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
151          355          360          365
153 ttg cgc tgg aag gaa ttc gtg cgg cgc cta ggg ctg agc gac cac gag 1152
154 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
155          370          375          380
157 atc gat cgg ctg gag ctg cag aac ggg cgc tgc ctg cgc gag gcg caa 1200
158 Ile Asp Arg Leu Glu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
159 385          390          395          400
161 tac agc atg ctg gcg acc tgg agg cgg cgc acg ccg cgg cgc gag gcc 1248
162 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
163          405          410          415
165 acg ctg gag ctg ctg gga cgc gtg ctc cgc gac atg gac ctg ctg ggc 1296
166 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
167          420          425          430
169 tgc ctg gag gac atc gag gag gcg ctt tgc ggc ccc gcc gcc ctc ccg 1344
170 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
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173 ccc gcg ccc agt ctt ctc aga tga 1368
174 Pro Ala Pro Ser Leu Leu Arg
175          450          455
178 <210> SEQ ID NO: 2
179 <211> LENGTH: 455
180 <212> TYPE: PRT
181 <213> ORGANISM: Homo sapiens
183 <400> SEQUENCE: 2
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185 1 5 10 15
187 Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro
188 20 25 30
190 His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
191 35 40 45
193 Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys

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DATE: 11/13/2002

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Input Set : A:\98385Iseq.txt

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194      50      55      60
196 Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
197 65      70      75      80
199 Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu
200      85      90      95
202 Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val
203      100      105      110
205 Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg
206      115      120      125
208 Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe
209      130      135      140
211 Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu
212 145      150      155      160
214 Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu
215      165      170      175
217 Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr
218      180      185      190
220 Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser
221      195      200      205
223 Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu
224      210      215      220
226 Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys
227 225      230      235      240
229 Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu
230      245      250      255
232 Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser
233      260      265      270
235 Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val
236      275      280      285
238 Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys
239      290      295      300
241 Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly
242 305      310      315      320
244 Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
245      325      330      335
247 Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp
248      340      345      350
250 Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro
251      355      360      365
253 Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu
254      370      375      380
256 Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln
257 385      390      395      400
259 Tyr Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala
260      405      410      415
262 Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
263      420      425      430
265 Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro
266      435      440      445

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RAW SEQUENCE LISTING

DATE: 11/13/2002

PATENT APPLICATION: US/09/898,234B

TIME: 15:47:18

Input Set : A:\98385Iseq.txt

Output Set: N:\CRF4\11132002\I898234B.raw

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273 <211> LENGTH: 483
274 <212> TYPE: DNA
275 <213> ORGANISM: Homo sapiens
277 <220> FEATURE:
278 <221> NAME/KEY: CDS
279 <222> LOCATION: (1)..(483)
281 <400> SEQUENCE: 3
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283 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser
284   1                      5                      10                      15
286 att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac tgt      96
287 Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys
288           20                      25                      30
290 cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc tcc      144
291 Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser
292           35                      40                      45
294 ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa      192
295 Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys
296   50                      55                      60
298 tgc cga aag gaa atg ggt cag gtg gag atc tct tct tgc aca gtg gac      240
299 Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp
300  65                      70                      75                      80
302 cgg gac acc gtg tgt ggc tgc agg aag aac cag tac cgg cat tat tgg      288
303 Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp
304           85                      90                      95
306 agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat ggg      336
307 Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly
308           100                      105                      110
310 acc gtg cac ctc tcc tgc cag gag aaa cag aac acc gtg tgc acc tgc      384
311 Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys
312           115                      120                      125
314 cat gca ggt ttc ttt cta aga gaa aac gag tgt gtc tcc tgt agt aac      432
315 His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn
316   130                      135                      140
318 tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att gag      480
319 Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile Glu
320 145                      150                      155                      160
322 aat                                                                483
323 Asn
326 <210> SEQ ID NO: 4
327 <211> LENGTH: 161
328 <212> TYPE: PRT
329 <213> ORGANISM: Homo sapiens
331 <400> SEQUENCE: 4
332 Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser
333   1                      5                      10                      15

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/898,234B

DATE: 11/13/2002
TIME: 15:47:19

Input Set : A:\98385Iseq.txt
Output Set: N:\CRF4\11132002\I898234B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:23; N Pos. 344,4157,5135,6255
Seq#:28; Xaa Pos. 4
Seq#:29; Xaa Pos. 7
Seq#:32; Xaa Pos. 1,2
Seq#:36; Xaa Pos. 6,10,11,12
Seq#:41; Xaa Pos. 9,10,11
Seq#:43; Xaa Pos. 6,18
Seq#:44; Xaa Pos. 16,17
Seq#:46; Xaa Pos. 7

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23
Seq#:1; Line(s) 24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43
Seq#:1; Line(s) 44,45,46,47,48,49,50,51,52,53,54,55,56,57,58,59,60,61,62,63
Seq#:1; Line(s) 64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79,80,81,82,83
Seq#:1; Line(s) 84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100,101,102
Seq#:1; Line(s) 103,104,105,106,107,108,109,110,111,112,113,114,115,116,117
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